-1-

## SEQUENCE LISTING

```
<110> Pharmacia AB
<120> Screening methods
<130> 00244
<140>
<141>
<160> 3
<170> PatentIn Ver. 2.1
<210> 1
<211> 460
<212> DNA
<213> Mus musculus
<300>
<308> GenBank / AA028416
<309> 1996-09-16
<400> 1
gccatggcgt tggggctgca gcgcgtgagg tcgaacaccg agctgcggaa ggagaagtcg 60
cgggaccgcc cgcagccggc gcacgaggag acggaggtgc tgtaccagct ggcgcacact 120
ctgccctttg cgcgcggcgt cacaccntnc tggacaaggc ctccatcatg cgcctcacaa 180
tragctacct gegratgace geetetgege acagantgga aaaaggggga gagccactgg 240
acgcctgcta cctgaaggcc ctggagggtt tcgtcatggt actcaccgcc gagggagaca 300
tggcttacct gtcggaaaat gtcagcaagc acctgggcct cagtcagtgg acctctgttc 360
ctcctccctg atacataacc ccactcctgg taccaatttc tctctggagc tcattggaca 420
cagtatettt gattttatea teeetgtgae caagaggaae
                                                                   460
<210> 2
<211> 1100
<212> DNA
<213> Mus musculus
<220>
<221> CDS
<222> (19)..(942)
<400> 2
gaatteggea egagggee atg geg ttg ggg etg eag ege gtg agg teg aac
                    Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn
                      1
acc gag ctg cgg aag gag aag tcg cgg gac gcg cgc cgc agc cgg cgc
                                                                   99
Thr Glu Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg
             15
age cag gag acg gag gtg ctg tac cag ctg gcg cac act ctg ccc ttt
                                                                   147
Ser Gln Glu Thr Glu Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe
         30
qcq cqc qqc qtc agc gcg cac ctg gac aag gcc tcc atc atg cgc ctc
                                                                   195
Ala Arg Gly Val Ser Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu
```

	: Ile					Met					Ālā				a aaa y Lys 75	243
					Gly					Glu					g ttt y Phe	291
cgt Arg	cat His	ggt Gly	act Thr 95	His	e cgc Arg	cga Arg	gly	aga Arg 100	His	ggc Gly	tta Leu	ı cct ı Pro	gto Val	. Gl <sub>3</sub>	a aaa / Lys	339
-	_		Ala				_			-			Ser		tcc Ser	387
															att Ile	435
														-	ctt Leu 155	483
			ctg Leu													531
_			gag Glu 175	_				_	_	_	_	_	_			579
			cgc Arg													627
			gga Gly													675
Pro 220	Ala	Gly	agc Ser	Pro	Arg 225	Ser	Glu	Pro	Pro	Leu 230	Gln	Суз	Leu	Val	Leu 235	723
atc Ile	tgt Cys	gaa Glu	gcc Ala	atc Ile 240	ccc Pro	cag Gln	ctc Leu	ccc Pro	ttc Phe 245	cac His	gat Asp	ggt Gly	gct Ala	act Thr 250	ctg Leu	771
			cag Gln 255				Pro									819
			cta Leu			Leu					Pro					867
cag Gln	385 385	aaa Lys	gjà aaa	act Thr	Glu	tcc Ser 290	tct ( Ser )	ctc Leu	ccc Pro	Ser	tgg Trp 295	gtg Val	ttg Leu	tgg Trp	gcc Ala	915
ctt Leu 300				Asn				tag	gagg	gagt	ga a	ggac	atgg	С		962

<210> 3 <211> 307 <212> PRT <213> Mus musculus <400> 3 Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn Thr Glu Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu 25 2.0 Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser 40 Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu 55 60 Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys Arg Gly Arg Ala Thr 70 75 Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe Arg His Gly Thr His 90 Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys Cys Gln Gln Ala Pro 100 105 110 Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser Leu Ile His Asn Pro 115 120 125 Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile Gly His Ser Ile Phe 135 130 140 Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr 150 155 Pro Arg Pro Asn Leu Ser Lys Lys Leu Glu Ala Pro Thr Glu Arg 165 170 His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr 180 185 190 Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu His Cys Ser Gly His 195 200 205 Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro 215 220 Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile 230 235 Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu Gly Leu Pro Gln Glu 245 250 Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu Trp Lys Ala Leu Leu 260 265 Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu Gln Gly Lys Gly Thr 275 280 285 Glu Ser Ser Leu Pro Ser Trp Val Leu Trp Ala Leu Asn Arg Lys Asn 290 295 300 Cys Pro Gly 305